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RAW SEQUENCE LISTING

DATE: 04/30/2002

PATENT APPLICATION: US/10/022,939

TIME: 15:52:23

Input Set : A:\19963ydb.txt

Output Set: N:\CRF3\04302002\J022939.raw

ENTERED

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4 <110> APPLICANT: Kendall, Richard L.
5      Thomas, Kenneth A.
6      Mao, Xianzhi
7      Tebben, Andrew
9 <120> TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
12 <130> FILE REFERENCE: 19963YDB
14 <140> CURRENT APPLICATION NUMBER: 10/022,939
15 <141> CURRENT FILING DATE: 2001-12-18
17 <150> PRIOR APPLICATION NUMBER: 09/483,539
18 <151> PRIOR FILING DATE: 2000-01-14
20 <150> PRIOR APPLICATION NUMBER: 09/098,707
21 <151> PRIOR FILING DATE: 1998-06-17
23 <150> PRIOR APPLICATION NUMBER: 60/050,962
24 <151> PRIOR FILING DATE: 1997-06-18
26 <160> NUMBER OF SEQ ID NOS: 8
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 4071
32 <212> TYPE: DNA
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38 cttacaatta aggctaatac aactcttcaa attacttgca ggggacagag ggacttggac      180
39 tggctttggc ccaataatca gagtggcagt gagcaaaggg tggaggtgac tgagtgcagc      240
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42 tacagatctc catttattgc ttctgttagt gaccaacatg gagtcgtgta cattactgag      420
43 aacaaaaaca aaactgtggt gattccatgt ctggggtcca tttcaaactc caacgtgtca      480
44 ctttgtgcaa gatacccaga aaagagattt gttcctgatg gtaacagaat ttcttgggac      540
45 agcaagaagg gctttactat tcccagctac atgatcagct atgctggcat ggtcttctgt      600
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53 gaagccacgg tgggggagcg tgtcagaatc cctgcgaagt accttggtta cccaccacca      1080
54 gaaataaaat ggtataaaaa tggaataccc cttgagtcca atcacacaat taaagcgggg      1140
55 catgtactga cgattatgga agtgagtga agagacacag gaaattacac tgtcatcctt      1200
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58 caaacgctga catgtacggt ctatgccatt cctccccgcg atcacatcca ctggtattgg 1380
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60 ccttgtgaag aatggagaag tgtggaggac ttccaggagg gaaataaaat tgaagttaat 1500
61 aaaaatcaat ttgctcta atgaaggaaaa aacaaaactg taagtaccct tgttatccaa 1560
62 gcggcaaatg tgtcagcttt gtacaaatgt gaagcgggca acaaagtcgg gagaggagag 1620
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66 cctgtttgca agaacttggg tactctttgg aaattgaatg ccaccatgtt ctctaatagc 1860
67 acaaatgaca ttttgatcat ggagcttaag aatgcatact tgcaggacca aggagactat 1920
68 gtctgccttg ctcaagacag gaagaccaag aaaagacatt gcgtggtcag gcagctcaca 1980
69 gtcctagagc gtgtggcacc cacgatcaca ggaaacctgg agaatacagac gacaagtatt 2040
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71 tttaaagata atgagaccct tgtagaagac tcaggcattg tattgaagga tgggaaccgg 2160
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102 agtgaggaag cagaactttt aaagctgata gagattggag tgcaaaccgg tagcacagcc 4020
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105 <210> SEQ ID NO: 2
106 <211> LENGTH: 1356
107 <212> TYPE: PRT

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108 <213> ORGANISM: Human
110 <400> SEQUENCE: 2
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113 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
114 20 25 30
115 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
116 35 40 45
117 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
118 50 55 60
119 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
120 65 70 75 80
121 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
122 85 90 95
123 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
124 100 105 110
125 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
126 115 120 125
127 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
128 130 135 140
129 Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
130 145 150 155 160
131 Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
132 165 170 175
133 Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
134 180 185 190
135 Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
136 195 200 205
137 Tyr Gln Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg Ile Tyr
138 210 215 220
139 Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
140 225 230 235 240
141 Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
142 245 250 255
143 Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
144 260 265 270
145 Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
146 275 280 285
147 Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
148 290 295 300
149 Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
150 305 310 315 320
151 Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
152 325 330 335
153 Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
154 340 345 350
155 Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
156 355 360 365
157 Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr

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158      370      375      380
159 Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
160 385      390      395      400
161 Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
162      405      410      415
163 Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
164      420      425      430
165 Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
166      435      440      445
167 Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
168      450      455      460
169 Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
170 465      470      475      480
171 Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
172      485      490      495
173 Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
174      500      505      510
175 Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
176      515      520      525
177 Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
178      530      535      540
179 Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
180 545      550      555      560
181 Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
182      565      570      575
183 Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
184      580      585      590
185 Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
186      595      600      605
187 Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
188      610      615      620
189 Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
190 625      630      635      640
191 Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
192      645      650      655
193 Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
194      660      665      670
195 Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
196      675      680      685
197 Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
198      690      695      700
199 Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
200 705      710      715      720
201 Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
202      725      730      735
203 Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
204      740      745      750
205 Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
206      755      760      765

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207 Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
208      770      775      780
209 Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly
210 785      790      795      800
211 Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His
212      805      810      815
213 Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
214      820      825      830
215 Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val
216      835      840      845
217 Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
218      850      855      860
219 Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
220 865      870      875      880
221 Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
222      885      890      895
223 Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
224      900      905      910
225 Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
226      915      920      925
227 Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
228      930      935      940
229 Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
230 945      950      955      960
231 Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
232      965      970      975
233 Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro
234      980      985      990
235 Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
236      995      1000      1005
237 Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys
238      1010      1015      1020
239 Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn
240 1025      1030      1035      1040
241 Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp
242      1045      1050      1055
243 Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met
244      1060      1065      1070
245 Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val
246      1075      1080      1085
247 Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser
248      1090      1095      1100
249 Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys
250 1105      1110      1115      1120
251 Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr
252      1125      1130      1135
253 Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr
254      1140      1145      1150
255 Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala

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VERIFICATION SUMMARY

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